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Risk mapping of heart and skeletal muscle inflammation in salmon farming

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ABSTRACT

Heart and skeletal muscle inflammation (HSMI) is an infectious disease causing losses to the Norwegian salmon farming industry due to increased mortality and high morbidity in infected salmon. The disease is listed as a notifiable disease on list 3 (national list) by the Norwegian Food Safety Authority. HSMI is believed to be a viral disease, but the association to the recently discovered Piscine reovirus (PRV) remains unclear. Undoubtedly, other factors interact to determine whether PRV-infected fish develop disease or not.

In this study, logistic regression was used to model the risk of an outbreak of HSMI at the cohort level, by including spatio-temporal risk factors. The data consisted of fish cohorts grown on geo-referenced farms from 2002 to 2010. The risk factors included were: infection pressure, cohort size (maximum number of fish), cohort index (smolt characteristics), cohort lifespan (months in sea) and a geo-index calculated as the position along a local polynomial regression line based on the longitude and latitude of each farm included in the study.

The results showed that the risk of developing HSMI increased with increasing cohort lifespan, increasing infection pressure and increasing cohort size, and was mostly low for cohorts grown on farms in Southern-Norway, high for farms in Mid-Norway and variable for farms in Northern-Norway (based on the geo-index). The final model was used to explore three different scenarios with regards to the risk of developing HSMI, and to calculate the probability for each cohort of developing HSMI, independent of their actual disease-status.

The model suggested that the probability of developing HSMI was much higher in Mid-Norway than in the rest of the country. Even though PRV seems to be widely distributed in the environment, the finding that infection pressure has a large influence on the probability of developing HSMI, suggests that it might be possible to reduce the number of clinical outbreaks, if measures are taken to reduce infection pressure. However, the prospects of controlling the spread of HSMI and reducing clinical outbreaks might be difficult because of indications of large distance spread of the disease.

1. Introduction

Heart and skeletal muscle inflammation (HSMI) is an infectious disease causing losses to the Norwegian salmon farming industry due to increased mortality and high morbidity in infected farmed Atlantic salmon (*Salmo salar*) (Kongtorp et al., 2004a, 2006). The disease has also been reported in the United Kingdom (Ferguson et al., 2005).

HSMI was first identified on the west coast of Norway in 1999 (Fig. 1), from moribund fish sampled and tested using routine diagnostics. These fish had a pathological presentation not previously described and thus it was believed that this was the appearance of a new disease (Kongtorp

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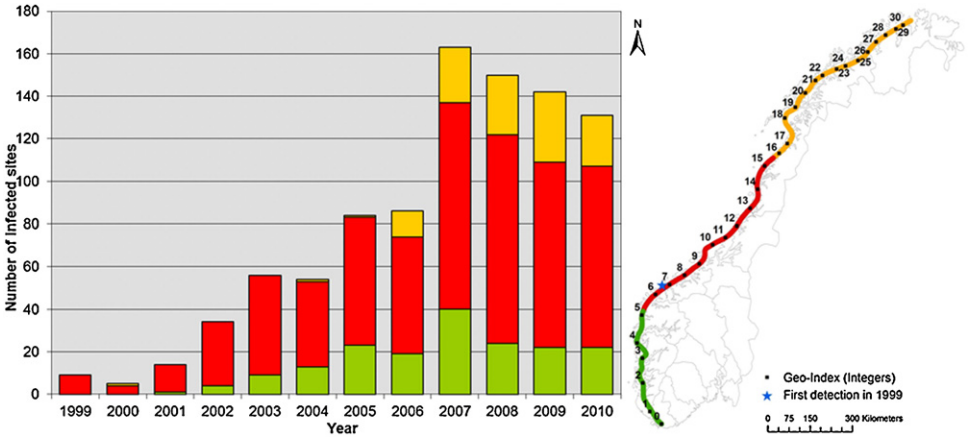

Fig. 1. Number of HSMI-diagnosed cohorts 1999–2010 and map showing the geo-index. Annual number of clinical outbreaks was collated from the laboratory information system of the NVI. Colours on the bars correspond to similar parts of the geo-index on the map: Green corresponds to a geo-index of less than 5.1, red denotes a geo-index of 5.1–15.7 and yellow indicates a geo-index above 15.7 (see text and Fig. 3c). Blue star on the map marks location for the first detection of HSMI in 1999.

et al., 2004b). Diagnosis of HSMI continues to be based on histopathological examination of organ samples with the finding of pathognomonic lesions (Kongtorp et al., 2004b).

After HSMI was first identified in Norwegian salmon farming, the number of clinical outbreaks in farms has increased and the affected geographical area has expanded (Fig. 1, data collated from the laboratory information system of the Norwegian Veterinarian Institute (NVI)). The rapid spread, together with the high morbidity associated with the disease, has led to HSMI being listed as a notifiable disease on list 3 (national list) by the Norwegian Food Safety Authority (NFSA) in 2008. This implies that HSMI diagnoses must be reported to the NFSA, who then have the mandate to impose restrictions on farms experiencing disease outbreaks (Anonymous, 2008). However, specific restrictions are currently not enforced for farms diagnosed with HSMI.

Previously, it has been demonstrated that the causative agent of HSMI is most likely a virus (Eliassen et al., 2004; Watanabe et al., 2006; Kongtorp and Taksdal, 2009). In 2010, a novel reovirus (piscine reovirus, PRV) was identified by the use of high-throughput DNA sequencing of heart tissue from HSMI infected fish (Palacios et al., 2010). This study demonstrated a strong association between PRV and HSMI. However, PRV was also found in clinically healthy fish, with comparably low virus levels (Palacios et al., 2010).

Aldrin et al. (2010) studied risk factors for outbreaks of HSMI in salmon cohorts and found that HSMI detections in previous fish cohorts at given farms was the single most important risk factor. HSMI diagnoses within shared contact networks and in nearby farms were additional important risk factors. The risk of developing HSMI was also elevated in autumn cohorts of smolts, compared to spring smolt cohorts (Aldrin et al., 2010).

A model investigating the effect of infection pressure on the probability of developing Pancreas disease (PD) in farmed cohorts of salmonids has been developed by Kristoffersen et al. (2009). Infection pressure for a given cohort, defined as exposure to infection by proximate infectious farms, had a relatively strong effect on the probability of recording a PD outbreak in a cohort. The model demonstrated that the probability of experiencing a PD outbreak in a given cohort of salmon was low if there were no neighbouring farms with PD, but increased as a function of increasing infection pressure (Kristoffersen et al., 2009).

In the present study, the model framework of Kristoffersen et al. (2009) was adapted to a dataset including all marine cohorts of farmed Atlantic salmon in Norway and all recorded cases of HSMI over the period 2002–2010. The aim of the study was to map important spatio-temporal risk factors for the development of HSMI in Norwegian salmon farming, in order to gain knowledge of their relevance to the possible control of the spread of this disease.

2. Methods

2.1. Data

2.1.1. Fish cohorts

Salmon farming consists of a freshwater phase of smolt production, followed by a marine grow-out phase. The marine production is conducted on certified farm sites authorized by the Directorate of Fisheries (DFF) and geo-referenced in the Aquaculture register (DFF; www.fiskeridir.no). The dominant practice for the marine production is that farms are stocked with cohorts of salmon smolts, which are then grown on this farm site until slaughtered. The farm is then fallowed for a period before stocking with a new cohort of smolts (see Kristoffersen et al., 2009). In the present study, only cohorts that were transferred to marine waters after December 2002 and slaughtered or moved before January 2011, and that were held on the same farm for at least six months, were included.

Cohorts where split into spring smolt cohorts, autumn smolt cohorts, mixed cohorts or relocated cohorts (cohort index) as described in Kristoffersen et al. (2009; Section 2.3).

All farms actively farming salmonids in marine waters must report key production statistics on a monthly basis

to the authorities. The data are collected in a database hosted by the Norwegian Food Safety Authority (NFSA). These statistics include stock numbers of fish and average fish weight. The data were obtained for all cohorts included in the present study, and pre-processed as described in Section 2.3 in Kristoffersen et al. (2009).

Cohort size was defined as the maximum number of fish in the cohort. Monthly biomass per cohort was calculated as average weight multiplied by the number of fish.

2.1.2. HSMI cases

A list of recorded HSMI cases during 2002–2010 on identified farms, including the month when samples were received at the NVI, was compiled from the laboratory information system at the NVI. The list of cases included all cases in which histopathological findings were consistent with HSMI, regardless of whether the overall conclusion from the case investigation was reported as suspected HSMI or confirmed HSMI. These cases all derived from samples that have been sent to the NVI in order to investigate elevated mortalities or other clinical disease signs. Before 2008, reporting HSMI was not compulsory, but reporting of elevated mortalities is mandatory and reasons for this must be investigated. Hence we believe that the list includes most of the HSMI cases. Furthermore, all Norwegian aquaculture production sites are required by legislation to undergo clinical inspections by fish health officers 6–12 times a year, depending on type of production (Anonymous, 2008). Therefore any case of HSMI that has not been reported by the farmer probably will be discovered at these inspections. Data from January 2003 to December 2010 were included in the regression analysis, while infection pressure was calculated based on data from 2002 to 2010.

Case cohorts were defined as cohorts with an HSMI diagnosis (as described in the case definition above) during their marine grow out phase, while control cohorts were defined as all other cohorts. In the dataset there were 1653 control cohorts and 608 case cohorts.

2.1.3. Geo-index

Based on all farm locations included in the study, a local polynomial regression line (loess; Cleveland et al., 1992) was calculated using farm longitudes as the dependent variable and latitudes as the independent variable (Fig. 1). Each farm was then projected onto the regression line and cohorts of fish associated with given farms were given a geo-index based on the position of the farm along the regression line, according to the expression:

$$\text{geo-index}_i = \sqrt{(\text{lat}_i - \text{lat}_{i-1})^2 + (f(\text{long}_i) - f(\text{long}_{i-1}))^2} + \text{geo-index}_{i-1},$$

where all farms were sorted based on their latitude. The geo-index of the first farm was defined as 0, lat_i was the latitude of farm i and $f(\text{long}_i)$ was the fitted longitude value of farm i along the regression line.

2.2. Methods

2.2.1. Infection pressure

It was assumed that a susceptible cohort is exposed to HSMI infection from all proximate cohorts on which there are infectious fish, dependent on the seaway distance between susceptible and infectious cohorts, d_{ij}. Calculation of seaway distance is described in Kristoffersen et al. (2009). Infection pressure was calculated based on the formula:

$$ip_i(t) = I_i(w_t) \times \sum_{j \in N_i(t)} \frac{I_j(t) x_j(t)}{d_{ij}} \quad (1)$$

where i was the cohort for which the infection pressure (ip_i) was calculated at month t, $I_i(w_t)$ was 1 if the fish at cohort i were susceptible and 0 otherwise, $N_i(t)$ was all active cohorts within a proximity of i in month t, $I_j(t)$ is 1 if cohort j was infectious at time t and 0 if not. Since it is not known for which distance HSMI is infectious, different levels of proximity were tested, by only including other cohorts within different predefined radii from the cohort. The different levels of proximity used in the study were 5, 10, 25, 50 and 100 km.

Different scenarios for the numerator $x_j(t)$ were tested: a constant term; the number of fish at cohort j in month t; and the biomass at cohort j in month t. A constant term in the numerator indicates that an infectious cohort in the neighbourhood is important, independent of the size of the infected cohort. Accounting for the number of fish or biomass in the numerator indicated that cohort infectiousness is dependent on the size of the fish stock.

How long a cohort was assumed infectious ($I_j(t)$) was tested in different scenarios. All scenarios assumed that fish were infectious 2 months prior to HSMI detection. However, since it is not known how long the fish are infectious after an HSMI diagnosis, the following post diagnosis levels were explored in this study: 2 months, 6 months and the remaining lifespan of cohorts.

Even though HSMI has been observed more often in relatively small fish (Kongtorp, 2009), it is not known if susceptibility to HSMI varies with size or age of the fish. Therefore, different restrictions on the maximum fish weight (w_t) for which possible exposure to infection were allowed, was explored. The following levels of fish weight were used: <0.5 kg, <1 kg, <2 kg and the entire cohort lifespan.

2.2.2. Statistical approach

Using logistic regression, differences between case and control cohorts were explored. The regression was done using generalized additive models (GAM) and splines allowing the relationships between the independent and the depended variables to be non-linear (Hastie and Tibshirani, 1996). The shape of the spline function was transformed into odds ratios prior to plotting. To compare the different infection pressure scenarios, univariate tests of logistic regressions of with each scenario were conducted and Akaike's Information Criterion (AIC) values between the models were compared. The scenario with lowest AIC value was used further in the multivariable analysis with other explanatory variables: cohort size; cohort

Table 1
Descriptive statistics for the potential risk factor variables for cohorts with and without HSMI diagnoses. The results of single variable logistic regressions are summarised by *p*-value and AIC.

Risk factor variables	Level	Control cohorts	Case cohorts	*p*-value	AIC
Infection pressure (10^6 fish km^{-1})	Mean	0.09	0.29	<0.001	2197
	(5%, 95%)	(0, 0.35)	(0, 0.89)		
	Sd	0.18	0.30		
Cohort size (10^3 fish)	Mean	594	867	<0.001	2473
	(5%, 95%)	(88, 1470)	(161, 1898)		
	Sd	499	593		
Cohort lifespan (months)	Mean	16.5	18.4	<0.001	2582
	(5%, 95%)	(7, 26)	(9, 25.6)		
	Sd	6.5	5.5		
Cohort index	Autumn smolt	289	180	<0.001	2599
	Spring smolt	611	290	<0.001	2615
	Relocated	518	84	<0.001	2560
	Mixed	235	54	<0.001	2624
Geo-index	Mean	10.1	10.2	<0.001	2388
	(5%, 95%)	(1.9, 26.0)	(1.9, 25.2)		
	Sd	7.7	6.2		

index; geo-index and cohort lifespan. Finally all scenarios of infection pressure were tested with the selected model and a final model was obtained. Based on the final model, the risk of HSMI diagnosis for increasing infection pressure was calculated for three different scenarios. In addition, the risk of developing HSMI for each cohort in the dataset was calculated. To measure the accuracy of the model, area under the curve (AUC) of a ROC curve was calculated. The ROC curve is a plot of the sensitivity versus (1 – specificity) for all thresholds.

3. Results

3.1. Descriptive statistics

The annual number of HSMI-diagnoses increased more than two-fold from 2003 to 2010, and the geographic distribution of diseased fish cohorts expanded both northward and southward from the index case in Mid-Norway (Fig. 1).

The median time from transfer of fish to marine waters to initial diagnosis of HSMI was 8 months (interquartile range: 2–15 months). Median cohort lifespan was 16.5 months for control cohorts and 18.4 months for case cohorts (Table 1). Comparing AIC values from the univariate logistic regression analyses showed that the variable infection pressure was the best predictor of case cohorts versus control cohorts, followed by geo-index and cohort size (Table 1).

3.2. Model fitting

Forward model selection resulted in a model including the variables infection pressure, cohort size, geo-index, log(cohort life span) and cohort index. Comparison of AIC values revealed that infectiousness throughout the remaining lifespan of infected cohorts outperformed infectiousness restricted to 2 or 6 months, when different scenarios for infection pressure were calculated. In all tests, using cohort size as the numerator outperformed using biomass or a constant term. Susceptibility to infection pressure restricted to a maximum fish size of 0.5 kg performed better than restrictions set at 1 kg, 2 kg or no such restriction (entire lifespan). AIC values for the different levels of neighbourhood for this model were 5 km: 2113.8, 10 km: 2064.2, 25 km: 2009.8, 50 km: 1998.0 and 100 km: 1997.6. Hence, proximity to infected cohorts equal to 50 or 100 km outperformed other neighbourhood proxies (Fig. 2).

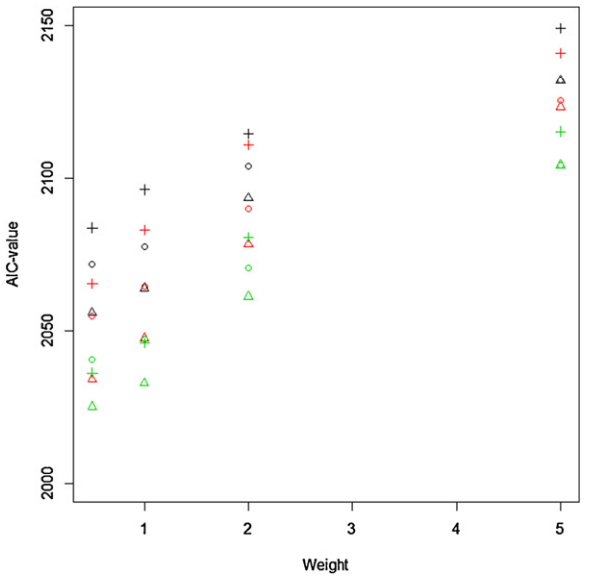

Fig. 2. AIC values for different infection pressure scenarios for the logistic regression by the final model. For the infection pressure the following different numerators were tested: constant (○), number of fish at cohort at a given time (Δ) and biomass at cohort at a given time (+). For infectious time the following levels are illustrated: 2 months (black), 6 months (red) and remaining lifespan (green). Neighbourhood was set at 100 km for all tests. The *x*-axis correspond to when fish on a cohort is assumed to be susceptible for infection, corresponding to <0.5 kg, 1 kg, 2 kg and the entire lifespan.

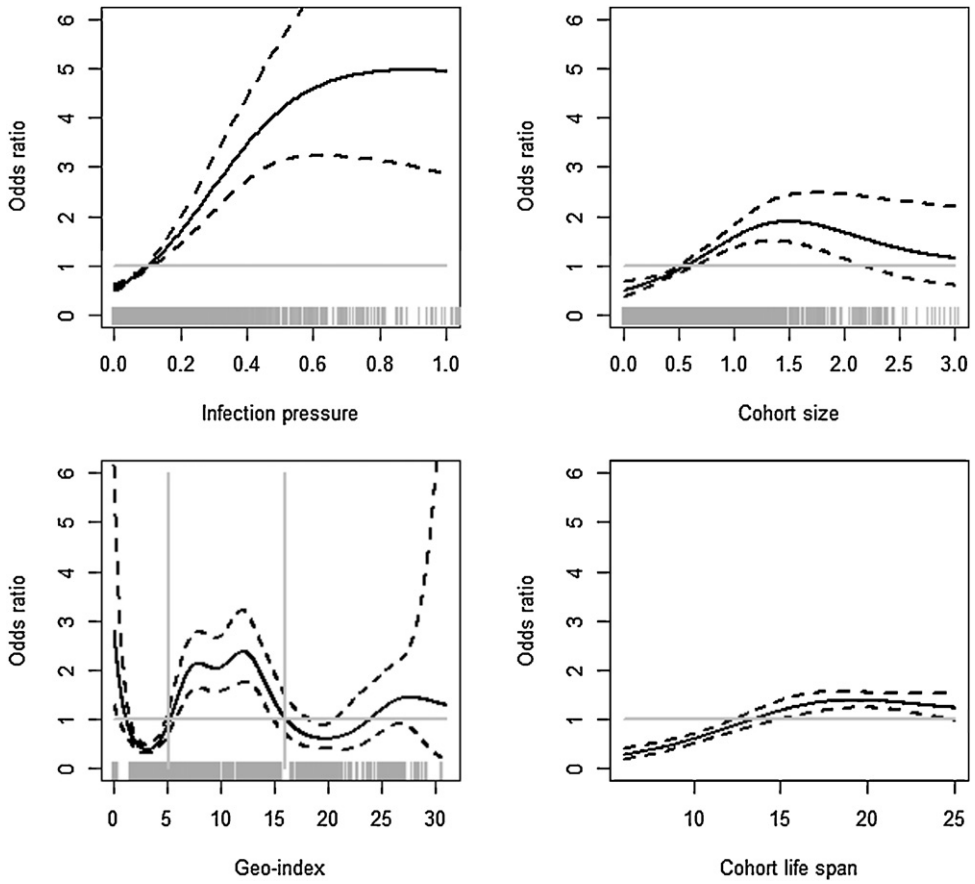

Fig. 3. Plots of the odds ratio of infection pressure (a), cohort size (b), geo-index (c), and cohort life span (d) as estimated in the logistic regression by the final model. Dashed lines represent 95% confidence intervals. Horizontal lines correspond to an odds ratio of 1. Vertical lines in (c) marks where geo-index contribute with lower probability of getting HSMI shifting to higher probability of getting HSMI and back, respectively.

3.3. Risk factors for outbreaks of HSMI

The odds ratio for developing HSMI was 0.6 (95% CI: 0.4–0.9) for mixed cohorts and 1.5 (95% CI: 1.1–1.9) for autumn smolt cohorts. The shapes of the odds ratio functions of the variables infection pressure, cohort size, geo-index and cohort lifespan are shown in Fig. 3. The risk of HSMI was low if the infection pressure was below approximately 0.1, but the odds increased to above 3, when the infection pressure increased to 0.5 (Fig. 3a). For cohorts with less than 0.5 million fish, the risk of HSMI was low. For cohorts larger than 0.5 million fish, the odds of HSMI increased, and was highest at 1.5 million fish (OR∼2). For cohorts larger than 1.5 million fish, the odds were between ∼1.2 and 1.8 (Fig. 3b) with wide confidence intervals due to few cohorts of this size. The risk of HSMI was mostly low for farms with a geo-index lower than 5.1 (South-Norway), high for farms with a geo-index between 5.1 and 15.7 (Mid-Norway) and variable for farms with a geo-index above 15.7 (Northern-Norway; Figs. 3c and 1). The risk of HSMI was significantly lower for cohort lifespans less than ∼13 months (Fig. 3d). The AUC for the ROC curve of the final model was 0.81.

The model was also used for predicting the risk of developing HSMI in cohorts given three different scenarios: (i) a large cohort (1.6 million fish) in Mid-Norway; (ii) a medium-sized cohort (0.56 million fish) in Mid-Norway; and (iii) a medium-sized cohort in South-Norway. In all scenarios, the cohort was chosen as a spring smolt cohort, the total cohort lifespan was fixed at 18 months (median in dataset), and the neighbourhood set to 100 km. For all three scenarios, the risk of developing HSMI increased when infection pressure increased from 0.0 to 0.3, and levelled off with infection pressure above 0.4 (Fig. 4). The simulation illustrates that the predicted risk of developing HSMI was around 10% higher for a large than a medium-sized cohort in Mid-Norway, when all other factors were kept constant. Similarly, the predicted risk was 15–30% lower for a cohort in Southern-Norway, compared to a cohort in Mid-Norway, when all other factors were kept constant (Fig. 4).

Finally, the model was used to calculate the risk of developing HSMI for each cohort, independent of their actual disease-status (Fig. 5). Cohorts terminated in 2003–2006, 2007–2008 and in 2009–2010, respectively, are shown together. The risk of developing HSMI in cohorts generally

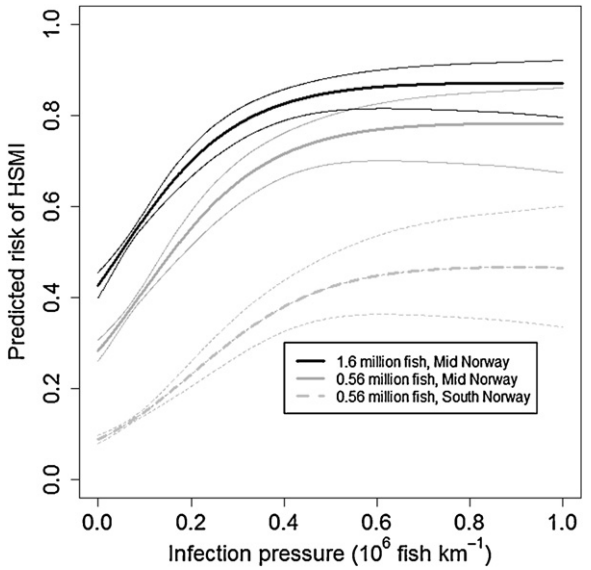

Fig. 4. Predicted risk of HSMI in a given cohort as a function of infection pressure for three different scenarios. Grey indicates medium-sized cohort (median, 0.56 million fish) and black large cohort (95% quantile, 1.6 million fish). Solid line: Mid-Norway, dashed line: Southern-Norway. In all scenarios the cohort was set to be a spring smolt cohort and cohort lifespan (the marine phase) was fixed to 18 months (median in dataset).

increased over time and space, portraying an emerging epidemic of HSMI in Norwegian salmon farming.

4. Discussion

This study presents an analysis of risk factors in space and time for the development of HSMI in farmed cohorts of Atlantic salmon in Norway. The results suggest that cohort exposure to infection, as measured by infection pressure from neighbourhood infectious farms, is an important risk factor. When susceptibility to infection pressure was restricted to small sized fish, the explanatory ability of infection pressure as a risk factor improved, indicating that salmon are critically susceptible to exposure at small sizes. A large scale spatial effect on the risk of developing HSMI was suggested by a geo-index variable characterising salmon farms. The risk of developing HSMI in cohorts generally increased over time and space, portraying an emerging epidemic of HSMI in Norwegian salmon farming.

Among the tested risk factors for HSMI diagnoses, the variable infection pressure was the best predictor of case cohorts versus control cohorts. This we interpret as a reflection of the contagious nature of this disease, which recently has been associated with piscine reovirus (PRV (Palacios et al., 2010)). A notable observation in this respect, however, is that PRV has been shown to have a wide geographical distribution (Garseth et al., in press) and been detected by PCR in various species of clinically healthy fish (Garseth et al., in press; Wiik-Nielsen et al., 2012). Nevertheless, clinical expression of HSMI has been associated with low PCR cycle threshold values, indicating high loads of viraemia (Løvoll et al., 2012). The present effect of infection pressure therefore indicates that the intensity of exposure to the disease agent plays a role in determining whether disease is induced, rather than merely exposure versus non-exposure. Both statistical modelling and experimental challenges have emphasized relationships between loads of viral exposure and disease development for aquatic viruses (Murray, 2009; Murray and Peeler, 2005; Rolland and Winton, 2003). What has been measured in this study is the risk of detecting clinical HSMI in cohorts of farmed fish, defined as the finding of pathological changes consistent with the disease. The significance of these histopathological findings is not overt, since the consequence of a HSMI-outbreak for the individual farms varies, and is difficult to measure on a larger scale as HSMI does not cause high mortality in the affected fish.

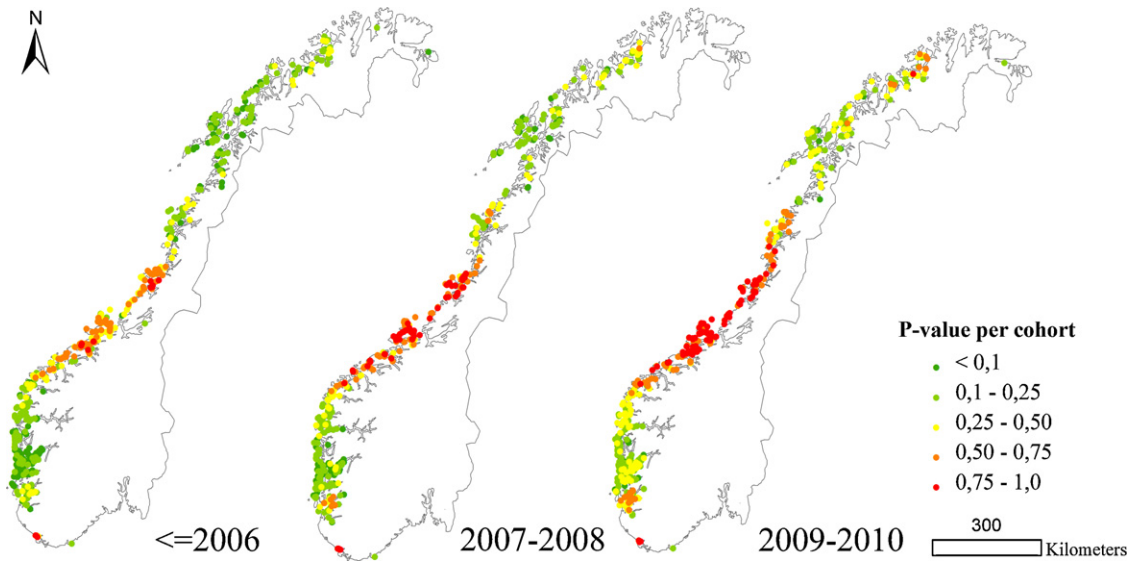

Fig. 5. Maps showing the risk per cohort for detection of HSMI according to the final model. The different maps shows cohorts terminated up to and including 2006, 2007–2008 and 2009–2010. Mixed and relocated cohorts were not included.

However, HSMI causes high morbidity: >80% of the fish are affected with heart lesions and an activated immune response (Kongtorp et al., 2006; Kongtorp and Taksdal, 2009). As a consequence, performances of the fish are impaired with regard to production and they are more prone to stress-induced mortality or infections with other agents. In this study, cases of HSMI were compared to controls which were cohorts that did not experience HSMI during their production period. Because of the mandatory health inspections, it is unlikely that HSMI outbreaks in cohorts of farmed fish would go unnoticed, and so the controls are believed to be true controls.

The present multivariable model performed significantly better in explaining HSMI development versus non-development when susceptibility to infection pressure was restricted to small fish (<0.5 kg). This suggests that small fish either are critically more susceptible to infection, or more prone to progressing from infection to disease. This could be related to stress associated with smolt transference from freshwater to marine waters (Kongtorp et al., 2006).

Distances of 50 or 100 km included in the neighbourhood when computing infection pressure gave the best model fit, implying that relatively distant infectious farms increase the risk of developing clinical HSMI. These distances far exceed inter-farm transmission distances suggested for other viral diseases, such as infectious salmon anaemia (Aldrin et al., 2011). We can only speculate on reasons for such long distance associations with regard to infection pressure. It could be due to transmission by other mechanisms than by water currents, e.g. by fomites or free roaming fish. Nevertheless, if HSMI does spread over large distances then the prospects of controlling disease spread are reduced.

In the present analysis we introduced a variable which we termed geo-index. This variable characterises each farm as projected onto a local polynomial regression line through the coordinates of all farms hosting cohorts of farmed salmon. A motivation for doing this was to ensure that excess spatial dependencies were accounted for, i.e. after having accounted for infection pressure. Marine salmon farms are located along the Norwegian coast from the north to the south (Fig. 3), implying that farm locations are well represented by the regression line and associated geo-indexes. Furthermore, since the polynomial regression line turns in different geographic directions according to farm locations along the coast, the present geo-indexes give higher geographical resolution for the salmon farms than either longitude or latitude on their own merit.

The geo-index was a significant risk factor for HSMI development in cohorts. With exception of a small group of farms in the south with geo-indexes close to zero, the risk associated with the geo-index was high in Mid-Norway and decreased northwards and southwards. The geo-index effect represents some second order spatial effect, adding to the spatial effect of infection pressure. Whereas the infection pressure captures local clustering of disease outbreaks, where the effect of an infectious farm is weighted according to distance to an exposed farm, the geo-index captures additional spatial effects on larger geographic scales. This can be interpreted as an effect of the area to which a given farm belongs, rather than the more dynamic distribution of infectious farm populations in the neighbourhood of a given farm, which is represented by infection pressure. The causal reason for the geo-index effect is unknown, but one explanation could be that the virus somehow establishes in the environment and can thus infect new fish cohorts that are put to sea. If so, this would yield a spatial effect on the risk of developing HSMI, regardless of infection pressure. Supporting this theory, Aldrin et al. (2010) demonstrated that if a farm had previous experience with HSMI in earlier cohorts, then 52% of subsequent cohorts developed HSMI. Furthermore, 91% of the HSMI outbreaks had a previous outbreak within the last year and within a 50 km radius (Aldrin et al., 2010). Since farms are fallowed and disinfected between cohorts, these studies indicate that there might be a reservoir of infection in the local environment. Another aspect is potential transmission between farmed and wild fish. Recently, Garseth and colleagues screened a large number of wild Atlantic salmon, and found that PRV is common (13.4% prevalence) (Garseth et al., in press). In addition, Wiik-Nielsen et al. (2012) investigated the prevalence of PRV in marine fish species. This latter study found PRV in four different marine fish species and in four separate locations widely spread along the Norwegian coast (Wiik-Nielsen et al., 2012). Since wild fish are attracted to fish farms (Dempster et al., 2009) and also migrate between fish farms (Uglem et al., 2009), it is possible that wild fish play a role in the transmission of PRV-virus and hence the spread of HSMI.

The geo-index effect could also be due to some spatial characteristic that is not related to transmission of the disease agent per se, but which affects the likelihood of diagnosing clinical HSMI. A trivial explanation would be some sort of geographical bias in the diagnostics of the disease. Even though we cannot rule this out, it does not seem a plausible explanation since all the diagnostics have been done by the Norwegian Veterinary Institute, which is a reference laboratory for fish diseases with unified criteria for HSMI conclusions.

The spatial effects measured by infection pressure and geo-index were the most important risk factors in our study, but we also found a significant effect of other risk factors. Cohorts that were put to sea in autumn had higher risk of HSMI than any other cohorts. This is consistent with was has been demonstrated by Aldrin et al. (2010), and is discussed there. Additionally, we found that mixed cohorts had lower risk of HSMI, which we speculate might be due to two aspects. According to Kristoffersen et al. (2009), fish in mixed cohorts have an average weight of 1 kg at sea transfer, rendering them less susceptible to disease according to the other results presented here. Further, since mixed cohorts are defined as having multiple introductions of fish, we would expect that only disease-free locations are used for this purpose, as fish are not introduced into farms with disease.

Cohorts with a shorter lifespan also had lower risk of HSMI. This is presumably because these cohorts consist mainly of relocated or mixed fish, that is, fish that have been put to sea at a higher weight, and therefore less susceptible to HSMI.

Further, low cohort size was protective against HSMI. Cohort size was also the best numerator for the infection pressure variable, suggesting that cohort number of fish was more important than biomass.

5. Conclusion

The present risk mapping of HSMI portrays an emerging disease in Norwegian salmon farming, spreading out from a focal area in Mid-Norway with increasing risks of developing disease in salmon cohorts over time. Even though PRV seems to be widely distributed in the environment, the finding that infection pressure has a large influence on the risk of developing HSMI suggests that it might be possible to reduce clinical outbreaks if measures are taken to reduce infection pressure. This could be achieved by removing diseased sites or by vaccination. As the disease agent has only recently been identified, no vaccine is available yet, but this will most likely change in the foreseeable future.

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